Thesis Title **Melioidosis and HLA Class II Association**

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Abstract

Melioidosis is an infectious disease caused by *Burkholderia pseudomallei*. The disease is endemic in southeast Asia and is the leading cause of death from community-acquired septicemia in northeastern Thailand. The bacteria enter the body via ingestion, inhalation or in association with trauma sustained in areas where the organism contaminates in surface soil and water. The very high rates of morbidity and mortality have been major problems for physicians in endemic areas. The manifestation and type of melioidosis, are influenced by immune response. Although the patients are infected with the same bacteria, they exhibit different clinical and pathological outcome. As the precise nature of host factors are poorly understood, it is interesting to see whether genetic factor play a role in governing the expression of the disease.

In this study, the distribution of HLA class II alleles were examined in 48 melioidosis patients which consisted of 27 septicemic melioidosis patients and 21

localized melioidosis patients, 48 other patients and 105 normal controls from northeastern Thailand. PCR amplification at the polymorphic second exon and sequence specific oligonucleotide (SSO) typing for DRB1, DQA1 and DQB1 were performed according to the 11th International Histocompatibility Workshop protocol using the Workshop SSO reagents.

The frequency of DRB1*(1501+1502+1602) was significantly increased in patients with melioidosis, of which DRB1*1501 was increased in localized melioidosis patients and DRB1*1602 was increased in septicemic melioidosis patients. For DQ loci, DQA1*0102, DQB1*0501 and DQ5 were increased in localized melioidosis patients, whereas, DQB1*03032 was decreased in melioidosis patients.

The analysis of HLA class II allele frequencies in melioidosis patients performed in this study could be beneficial in furthering our understanding of the immunogenetic basis of the pathology of melioidosis and perhaps other diseases in Thailand.